



SEQUENCE LISTING

<110> Kilian, Andrzej
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
THEREOF

<130> 191106.407C2

<140> 09/502,498
<141> 2000-02-11

<160> 155

<170> PatentIn Ver. 2.0

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<212> DNA
<213> Homo sapiens

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115	120	125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val		
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Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val		
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Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr		
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Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly		
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Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg		
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Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg		
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Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg		
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Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp		
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Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val		
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Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His		
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Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro		
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Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser		
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370	375	380
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Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu			
435	440	445	
Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe			
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Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser		
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Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe		
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Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly		
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Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp		
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Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr		
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Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser		
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Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr		
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Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala		
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Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys		
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Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu		
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Val Glu Leu Leu Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln		
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Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
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Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
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Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
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Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
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Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
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Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly
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Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro
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Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu
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Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
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His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
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His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
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Ala Arg Arg Arg Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
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Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
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Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
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Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
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Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
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Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
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Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
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Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
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Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
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Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
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Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
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Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
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Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
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Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
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Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
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Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
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Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
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Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
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Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
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Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
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Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
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Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 755 760 765

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 770 775 780

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 785 790 795 800

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 805 810 815

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 820 825 830

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 835 840 845

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 850 855 860

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 865 870 875 880

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 885 890 895

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 900 905 910

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 915 920 925

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 930 935 940

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 945 950 955 960

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 965 970 975

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 980 985 990

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 995 1000 1005

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1010 1015 1020

Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1025 1030 1035 1040

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1045 1050 1055

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1060 1065 1070

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1075 1080 1085

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1090 1095 1100

<210> 5
 <211> 884
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
 1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn

20

25

30

Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
 35 40 45

Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
 50 55 60

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65 70 75 80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
 85 90 95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
 100 105 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
 115 120 125

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
 130 135 140

Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
 145 150 155 160

Trp Val Gln Arg Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
 165 170 175

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190

Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205

Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220

Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240

Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255

Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270

His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285

Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300

Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro
 305 310 315 320

Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu

325	330	335
Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His 340	345	350
Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu 355	360	365
Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr 370	375	380
Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp 385	390	395
Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu 405	410	415
Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn 420	425	430
Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu 435	440	445
Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe 450	455	460
Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys 465	470	475
Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile 485	490	495
Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg 500	505	510
Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys 515	520	525
Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met 530	535	540
Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg 545	550	555
Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn 565	570	575
Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp 580	585	590
Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val 595	600	605
Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr 610	615	620
Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile		

625	630	635	640
Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys			
645	650	655	
Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe			
660	665	670	
Leu Ile Ile Ser Thr Asp Gln Gln Val Ile Asn Ile Lys Lys Leu			
675	680	685	
Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys			
690	695	700	
Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe			
705	710	715	720
Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser			
725	730	735	
Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile			
740	745	750	
Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr			
755	760	765	
Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp			
770	775	780	
His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp			
785	790	795	800
Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln			
805	810	815	
Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp			
820	825	830	
Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu			
835	840	845	
Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu			
850	855	860	
Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile			
865	870	875	880
His Ile Val Asn			

<210> 6
 <211> 13
 <212> DNA
 <213> Homo sapiens

<220>

<221> intron
 <222> (8)..(13)
 <223> First six bases of Y intron

<400> 6
 ccaggtggc ctc

13

<210> 7
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last seven bases of intron Y

<400> 7
 gcaggtgtcc tgcc

14

<210> 8
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron 1

<400> 8
 aaagagggtg gctg

14

<210> 9
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron 1

<400> 9
 aacagaagcc gagc

14

<210> 10
 <211> 14
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron Alpha

<400> 10

tgtcaaggtg gatg	14
<210> 11	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (1)..(7)	
<223> Last 7 bases of Intron Alpha	
<400> 11	
cccccaggac aggc	14
<210> 12	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (8)..(14)	
<223> First 7 bases of Intron Beta	
<400> 12	
gagccacgtc tcta	14
<210> 13	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (1)..(7)	
<223> Last 7 bases of Intron Beta	
<400> 13	
ggggcaagtc ctac	14
<210> 14	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (8)..(14)	
<223> First 7 base of Intron 2	
<400> 14	
actccaggtg agcg	14
<210> 15	
<211> 14	
<212> DNA	

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(7)

<223> Wherein N is any nucleotide

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron 2

<400> 15

nnnnnnnnctta tgcc

14

<210> 16

<211> 173

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(166)

<223> Full Sequence of Intron 3

<400> 16

aacgcagccg aagaaaacat ttctgtcggt actcctgcgg tgcttgggtc gggacagcca 60
 gagatggagc caccggcag accgtcggt gtggcagct ttccgggtc tcctggagg 120
 ggagttgggc tgggcctgtg actcctcagc ctctgtttc ccccaggat gtc 173

<210> 17

<211> 46

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 1 5 10 15

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 20 25 30

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 35 40 45

<210> 18

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Y

<400> 18

ggcctccccc gggctggcggt ccggctgggg ttgagggcgg ccggggggaa ccagcgacat 60
 gcggagagca ggcgaggcga ctcagggcgc ttcccccgca ggtg 104

<210> 19
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame One of Intron Y

<400> 19
Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly
1 5 10 15
Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
20 25 30

Arg Arg

<210> 20
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Two of Intron Y before termination
Codon

<400> 20
Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly
1 5 10

<210> 21
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<223> Reading Frame Two of Intron Y after termination
Codon

<400> 21
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15
Gln Gly Ala Ser Pro Ala Gly
20

<210> 22
<211> 34
<212> PRT
<213> Homo sapiens

<220>

<223> Reading Frame Three of Intron Y

<400> 22
 Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
 1 5 10 15
 Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro
 20 25 30
 Gln Val

<210> 23

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 1

<400> 23

gtggctgtgc tttggttaa cttcctttt aaccagaa 38

<210> 24

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 1 Translation

<400> 24

Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
 1 5 10

<210> 25

<211> 36

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Alpha

<400> 25

gtggatgtga cgggcgcgta cgacaccatc ccccaag 36

<210> 26

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> Intron Alpha Translation

<400> 26

Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
 1 5 10

<210> 27
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron Beta

<400> 27
 gtctctaccc tgacagaccc ccagccgtac atgcgacagt tcgtggctca cctgcaggag 60
 accagccgc tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc 120
 agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgcccgtgcg catcaggggc 180
 aa 182

<210> 28
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Intron Beta Translation

<400> 28
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 1 5 10 15

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 20 25 30

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 35 40 45

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 50 55 60

<210> 29
 <211> 226
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Intron 2

<400> 29
 gtgagcgcac ctggccggaa gtggagcctg tgcccgctg gggcaggtgc tgctgcagg 60
 ccgttgcgtc cacctctgct tccgtgtgg gcaggcact gccaatccca aagggtcaga 120
 tgccacaggg tgccctcgat cccatctgg gctgagcaca aatgcatctt tctgtggag 180
 tgagggtgcc tcacaacggg agcagtttc tgtgtatattt tggtaa 226

<210> 30
 <211> 159
 <212> DNA

<213> Homo sapiens

<220>

<223> Intron 3

<400> 30

ccgaagaaaa catttctgtc gtgactcctg cggtgcttgg gtcgggacac ccagagatgg 60
 agccaccccg cagaccgtcg ggtgtggca gcttccgt gtctccttgg aggggagttg 120
 ggctggccct gtgactcctc agcctctgtt ttccccag 159

<210> 31

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 3 Translation

<400> 31

Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
 1 5 10 15

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
 20 25 30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 35 40

<210> 32

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<223> Intron X. Complete length unknown

<400> 32

gacagtacc aggggggttg accgcggac tggcgccc cagggttgc tataggacca 60
 ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
 cgtggcccg ggcattggcct tctcggtgtg ctgcctggg tgccctgagc cctcaactgag 180
 tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240
 cctcctgagg ggctcttat tg 262

<210> 33

<211> 218

<212> DNA

<213> Homo sapiens

<220>

<223> Partial Sequence of Genomic Intron (approximately
 2.7 kb)

<400> 33

gtggctgtgc tttggtttaa cttcctttt aaccagaagt gcgtttgagc cccacatgg 60
 gatatcgtttt agatgaaggg cccggaggag gggccacggg acacagccag ggccatggca 120
 cggcgccac ccatttgtc gcacagttag gtggccgagg tgccgtgcc tccagaaaag 180

cagcgtgggg gtgttaggggg agtcctggg gcagggac

218

<210> 34

<211> 2031

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1767)..(1769)

<223> Wherein N is A, C, G or T

<220>

<223> N-Terminal Truncated Telomerase

<400> 34

Hypn

atggccgcgc ctcccgctg ccgagccgtg cgctccctgc tgcgcaagcca ctacgcgcgag 60
gtgctggccgc tggccacgtt cgtgcggcgc ctggggccccc aaggctggcg gctgggtgcag 120
cgccggggacc cggcgcttt cccgcgcgtg gtggggccagt gcctgggtgt cgtccctgg 180
gacgcacggc cggcccccgc cggcccttc ttccgcagg tgcctgcgtt gaaggagctg 240
gtggcccgag tgcgtcgagag gctgtgcgag cgcgcgcga agaacgtgt ggccttcggc 300
ttcgcgtgc tggacggggc cccgcggggc ccccccggg cttcaccac cagcgtgcgc 360
agctacactgc ccaacacggt gaccgcgcga ctggggggg gcccgcgtg gggctgctg 420
ctgcgcgcgc tgggcgcga cgtgctggg cacctgctgg cacgcgtgcgc gctttgtg 480
ctggtggtctc ccagctgcgc ctaccagggtg tgcggccgc cgcgttacca gtcggcgct 540
gcaactcagg cccggggccc gccacacgct agtgaccccc gaaggcgctt gggatgcgaa 600
cgggccttgg accatagcg tggggggcc ggggtcccc tgggcctgccc agcccccgggt 660
gcgaggaggc gccccggcag tgccagccga agtctccgt tgcccaagag gcccaggcg 720
ggcgctgccc ctgagccggc gccgcgcgc gttggccagg gtcctggc ccacccgggc 780
aggacgcgtg gaccgagtga cctgtggttc tgcgtgggtt cacctgcac accccgcgaa 840
gaagccaccc ttttggggg tgcgtctctt ggcacgcgc acctccaccc atccgtggc 900
cgccagcacc acgcggggcc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
tgcgtccccgg tgcgtccca gaccaagcac ttccctact ctcaggcga caaggagcg 1020
ctgcggccct ctttccact cagctctcg aggcccagcc tgactggcgc tcggaggctc 1080
gtggagacca ttttctggg tccaggccc tggatgcac ggcactcccg cagttgccc 1140
cgccctgccc agcgtactg gcaaatgcgg cccctgtttc tggagctgt tggaaccac 1200
gcccgtgc cctacggggt gtcctcaag acgcactgccc cgctgcgcgc tgccgtcacc 1260
ccagcagccc gtgtctgtgc cccggggaaag ccccaaggct ctgtggggc ccccgaggag 1320
gaggacacag accccgcgtg cttgggtcgat ctgcgtccgc agcacagcg cccctggcag 1380
gtgtacggct tgcgtggggc tgcgtcgcc cggctggc ccccaaggct ctggggctcc 1440
aggcacaacg aacgcgcgtt ctcaggaaac accaagaat tcatctccct ggggaagcat 1500
gccaagctct cgctgcaggc gtcgtacgtt aagatgagcg tgcgggactg cgctggctg 1560
cgccaggagcc cagggttgg ctgtgttccg gcccgcgc accgtctcg tgaggagatc 1620
ctggccaagt tccgtcaactg gtcgtatgtt gtcgtacgtt cgcgttgc caggctttc 1680
ttttatgtca cggagaccac gttcaaaaag aacaggctt tttctaccg gaagagtgtc 1740
tggagcaagt tgcaaaagcat tggaaatnnn acagtcacca ggggggttga ccggccgact 1800
ggcgctcccc agggttgact ataggaccag gtcgtccagg gcccgtcaag tagagggct 1860
ctcagaggcg tctggctggc atgggtggac gtcgtggggc gcatggcctt ctgcgtgtgc 1920
tgccgtgggt gcccgtggcc ctcactgagt cgggtggggc ttgtggctt ccgtgagctt 1980
ccccctagtc tggatgttccg ctgagcaagc ctcactgagg gtcgttctatt g 2031

<210> 35

<211> 588

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Predicted by SEQ ID NO:34

<400> 35
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 18 5 10 15
His (Thr) Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 580 585

<210> 36
 <211> 2041
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Intron 1 Addition

<400> 36
 atgcccgcgc ctccccgtg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgctgccc tggccacgtt cgtgcggcgc ctggggccccc agggctggcg gctggtcag 120
 cgcggggacc cggcgccgtt ccgcgcgcgtg gtggcccagt gcctgggtgt cgtccctgg 180
 gacgcacggc cgccccccgc cgccccctcc ttcccgcagg tgcctgcgtt gaaggagctg 240
 gtggcccgag tgcgcagag gctgtgcgag cgccgcgcga agaacgtgt ggccttcggc 300
 ttgcgcgtgc tggacggggc cgcgggggc ccccccgggg ccttcaccac cagcgtgcgc 360
 agctacactgc ccaacacggt gaccgacgcga ctgcggggga gcggggcgtg gggctgtg 420
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 <211> 670
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1; Encoded by SEQ ID NO:36

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 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe
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Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
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<210> 38

<211> 2541

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 2; Alpha Intron Addition

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 aaccttcctc aggaccctgg tccgaggtgt ccctgagttat ggctgcgtgg tgaacttgcg 2520
 gaagacagtgtgacttcc c 2541

<210> 39
 <211> 806
 <212> PRT
 <213> Homo sapiens

<220>
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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser Val Leu Arg Pro Val Pro Gly
 755 760 765

Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu
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Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala
 785 790 795 800

Ala Pro Ala Phe Val Gly
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<211> 3396
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Reference Telomerase; with Intron Alpha and Beta

<400> 40

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<210> 41
 <211> 3069
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3; with Introns Alpha, Beta and
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<400> 41

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 aggacgcgtg gaccgagtga ccgtgtttc tgcgtgtgtt cacctgcac accccgcgaa 840
 gaagccaccc tttggaggg tgcgtctct ggcacgcgc actccccc accgcgtggc 900
 cggcagcacc acgcggggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
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 ccagcagccg gtgtctgtc cccggaggaa gcccagggtt ctgtggcgc ccccgaggag 1320
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 cagatgccgg cccacggcctt attccctgg tgccgcctgc tgctggatc ccggaccctg 2820
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 ctggggcagg tgctgtgca gggccgttgc gtccacctct gcttccgtgt ggggcaggcg 2940
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3; Encoded by SEQ ID NO:41

<400> 42
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925

Pro Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940

Asp Tyr Ser Arg
 945

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 <211> 3362
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Altered C-terminus Protein; with Intron Alpha,
 Beta and 3

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 ctgttcagcg tgcgtcaacta cgagcggggcg cggcccccgc gcctctggg cgcctctgtg 2040
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 gtgggcagct ttccgggttcc tccgtggagg ggagttgggc tgggcctgtt actccctcagc 3300
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 ga 3362

<210> 44
 <211> 1096
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Altered C-terminus Protein; Encoded by SEQ ID
 NO:43

<400> 44
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560

Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
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Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
 995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Asn
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Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met
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 1075 1080 1085

Gly Arg Gly Val Gly Leu Gly Leu
 1090 1095

<210> 45

<211> 3918

<212> DNA

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; with Intron Beta

<400> 45

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TAC

!!

tyrosine

!!

Y

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<210> 46
 <211> 1120
 <212> PRT

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; Encoded by SEQ ID
NO:45

<400> 46

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35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
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 Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
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 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
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 545 550 555 560
 Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
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 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 705 710 715 720
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 725 730 735
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 805 810 815
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 820 825 830
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
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 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 850 855 860
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
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 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 900 905 910
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
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 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 930 935 940
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 945 950 955 960
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 965 970 975
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 980 985 990
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 995 1000 1005
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1010 1015 1020
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
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 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1045 1050 1055
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
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 1075 1080 1085
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<210> 47
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 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein that lacks Motif A; with Introns

Beta and 2

<400> 47

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<210> 48

<211> 936

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein that lacks Motif A; Encoded by
SEQ ID NO:47

<400> 48

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35 40 45Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
100 105 110Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
130 135 140Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val

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275	280	285	
Leu Ser Gly Thr Arg His Ser His	Pro Ser Val	Gly Arg Gln His His	
290	295	300	
Ala Gly Pro Pro Ser Thr Ser Arg	Pro Pro Arg Pro Trp	Asp Thr Pro	
305	310	315	320
Cys Pro Pro Val Tyr Ala Glu Thr	Lys His Phe Leu Tyr	Ser Ser Gly	
325	330	335	
Asp Lys Glu Gln Leu Arg Pro Ser	Phe Leu Leu Ser	Ser Leu Arg Pro	
340	345	350	
Ser Leu Thr Gly Ala Arg Arg	Leu Val Glu Thr Ile	Phe Leu Gly Ser	
355	360	365	
Arg Pro Trp Met Pro Gly Thr	Pro Arg Arg Leu	Pro Arg Leu Pro Gln	
370	375	380	
Arg Tyr Trp Gln Met Arg Pro	Leu Phe Leu Glu	Leu Leu Gly Asn His	
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Ala Gln Cys Pro Tyr Gly Val	Leu Leu Lys Thr	His Cys Pro Leu Arg	
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Ala Ala Val Thr Pro Ala Ala	Gly Val Cys Ala	Arg Glu Lys Pro Gln	
420	425	430	
Gly Ser Val Ala Ala Pro Glu	Glu Asp Thr Asp	Pro Arg Arg Leu	
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Val Gln Leu Leu Arg Gln His	Ser Ser Pro Trp	Gln Val Tyr Gly Phe	
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500	505	510	
Ser Val Arg Asp Cys Ala Trp	Leu Arg Arg Ser	Pro Gly Val Gly Cys	
515	520	525	
Val Pro Ala Ala Glu His Arg	Leu Arg Glu Glu	Ile Leu Ala Lys Phe	
530	535	540	
Leu His Trp Leu Met Ser Val	Tyr Val Val	Glu Leu Leu Arg Ser Phe	
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Phe Tyr Val Thr Glu Thr	Phe Gln Lys Asn	Arg Leu Phe Phe Tyr	

565

570

575

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 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 705 710 715 720

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 725 730 735

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 740 745 750

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 755 760 765

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 770 775 780

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 785 790 795 800

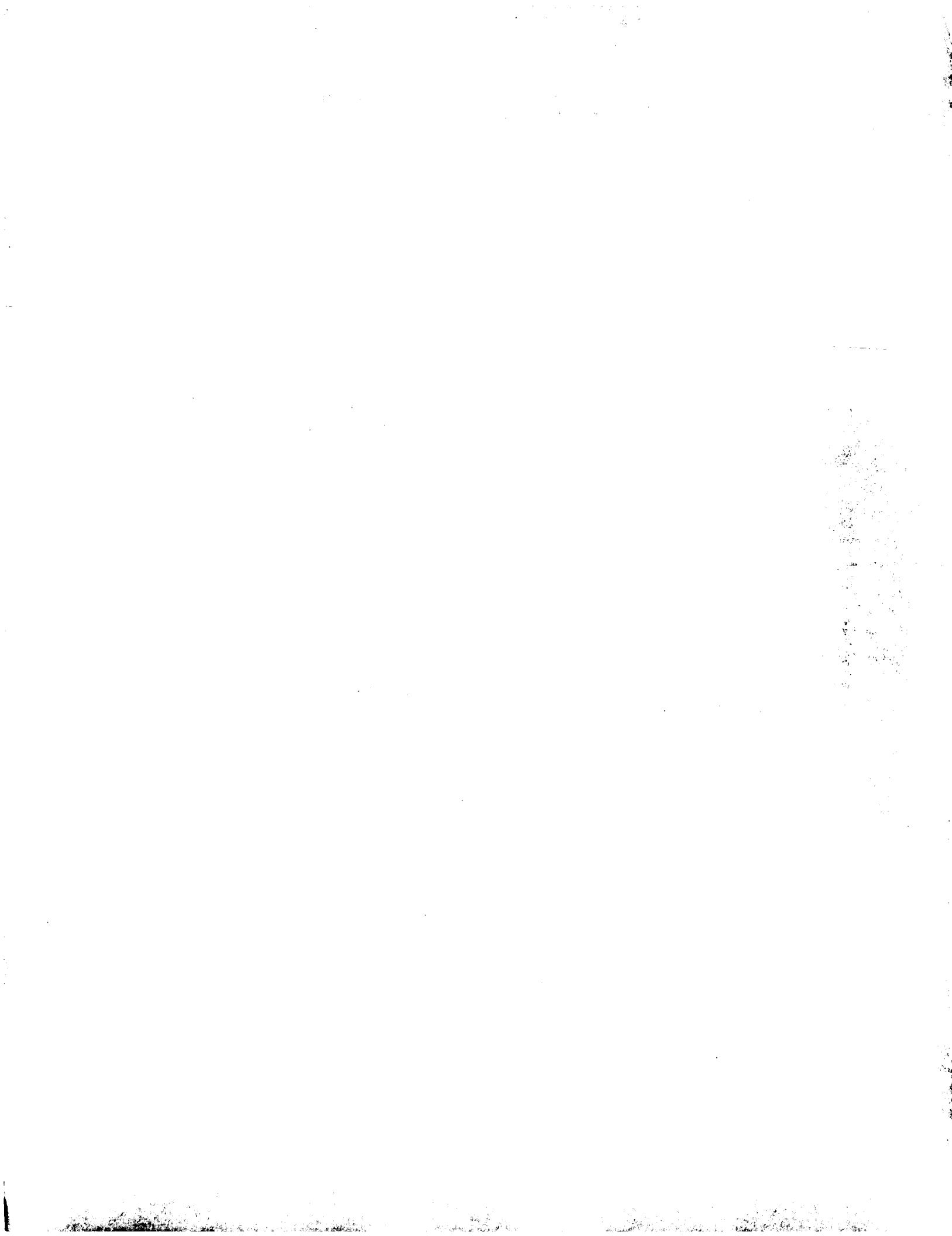
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Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 835 840 845

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 850 855 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro



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<210> 50

<211> 1084

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus;
Encoded by SEQ ID NO:49

<400> 50

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

115	120	125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val		
130	135	140
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val		
145	150	155
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr		
165	170	175
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly		
180	185	190
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg		
195	200	205
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg		
210	215	220
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg		
225	230	235
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp		
245	250	255
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val		
260	265	270
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala		
275	280	285
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His		
290	295	300
Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro		
305	310	315
320		
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly		
325	330	335
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro		
340	345	350
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser		
355	360	365
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln		
370	375	380
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His		
385	390	395
400		
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg		
405	410	415
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln		

420	425	430	
Gly Ser Val Ala Ala Pro Glu	Glu Glu Asp Thr Asp	Pro Arg Arg Leu	
435	440	445	
Val Gln Leu Leu Arg Gln His	Ser Ser Pro Trp Gln	Val Tyr Gly Phe	
450	455	460	
Val Arg Ala Cys Leu Arg	Arg Leu Val Pro Pro	Gly Leu Trp Gly Ser	
465	470	475	480
Arg His Asn Glu Arg Arg	Phe Leu Arg Asn Thr	Lys Lys Phe Ile Ser	
485	490	495	
Leu Gly Lys His Ala Lys	Leu Ser Leu Gln Glu	Leu Thr Trp Lys Met	
500	505	510	
Ser Val Arg Asp Cys Ala	Trp Leu Arg Arg	Ser Pro Gly Val Gly Cys	
515	520	525	
Val Pro Ala Ala Glu His	Arg Leu Arg Glu Glu	Ile Leu Ala Lys Phe	
530	535	540	
Leu His Trp Leu Met	Ser Val Tyr Val Val	Glu Leu Leu Arg Ser Phe	
545	550	555	560
Phe Tyr Val Thr Glu Thr	Phe Gln Lys Asn Arg	Leu Phe Phe Tyr	
565	570	575	
Arg Lys Ser Val Trp Ser	Lys Leu Gln Ser Ile	Gly Ile Arg Gln His	
580	585	590	
Leu Lys Arg Val Gln Leu	Arg Glu Leu Ser Glu	Ala Glu Val Arg Gln	
595	600	605	
His Arg Glu Ala Arg Pro	Ala Leu Leu Thr Ser	Arg Leu Arg Phe Ile	
610	615	620	
Pro Lys Pro Asp Gly	Leu Arg Pro Ile Val	Asn Met Asp Tyr Val Val	
625	630	635	640
Gly Ala Arg Thr Phe Arg	Arg Glu Lys Arg Ala	Glu Arg Leu Thr Ser	
645	650	655	
Arg Val Lys Ala Leu Phe	Ser Val Leu Asn Tyr	Glu Arg Ala Arg Arg	
660	665	670	
Pro Gly Leu Leu Gly Ala	Ser Val Leu Gly	Leu Asp Asp Ile His Arg	
675	680	685	
Ala Trp Arg Thr Phe Val	Leu Arg Val Arg Ala	Gln Asp Pro Pro Pro	
690	695	700	
Glu Leu Tyr Phe Val Lys	Asp Arg Leu Thr	Glu Val Ile Ala Ser Ile	
705	710	715	720
Ile Lys Pro Gln Asn Thr	Tyr Cys Val Arg	Arg Tyr Ala Val Val Gln	

725	730	735
Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser 740	745	750
Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu 755	760	765
Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser 770	775	780
Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe 785	790	795
Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys 805	810	815
Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu 820	825	830
Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp 835	840	845
Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His 850	855	860
Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro 865	870	875
Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro 885	890	895
Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala 900	905	910
His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu 915	920	925
Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala 930	935	940
Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg 945	950	955
Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp 965	970	975
Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile 980	985	990
Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro 995	1000	1005
Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile 1010	1015	1020
Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala		

1025 1030 1035 1040

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
1075 1080

<210> 51
<211> 2135
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1871)..(1873)
<223> Wherein N is A, C, G or T

<220>
<223> N-Terminal Truncated Telomerase (ver. 2); with
Intron Y

<400> 51
atgccgcgc ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgtgcgc tggccacgtt cgtgcggcgc ctggggccccc agggctggcg gctgggtcgag 120
cgcggggacc cggcgcttt cgcgcgcgtg gtggcccgat gcctgggtgtg cgtgcctgg 180
gacgcacggc cgcgcgcgcgc cgcgcgcgcgc ttccgcagg tgggcctccc cggggtcggc 240
gtccggctgg ggttggggc ggcggggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gttcccccg cagggtgtctt gcctgaaggaa gctggtgccc cgagtgtgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggccccgcgg gggccccccc gagggccttca ccaccagcgt gcgcagctac ctgccccaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtggggct gctgctgcgc cgcgtggcg 540
acgacgtgtc gttcacctg ctggcacgt gcgcgcgtt tggctgggt gctcccaact 600
gcgcctacca ggtgtgcggg cgcgcgtgtt accagctcg cgcgcact caggccccggc 660
ccccgcacca cgctagtggc ccccgaaaggc gtctggatg cgaacggggc tggaaaccata 720
gcgtcaggga ggcgggggtc cccctggggc tgccagcccc gggtgcggagg aggccggggg 780
gcagtgcaccc cgcgaatctg ccgttgcaca agagccccag gcgtggcgct gcccctgagc 840
cgagacggac gcccgttggg cagggggtctt gggcccaccc gggcaggacgc cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctcttgg 960
agggtgcgtc ctctggcacg cgcactccc accatccgt gggccgcac caccacgcgg 1020
gcgcgcgcgc cccatgcgcg ccaccacgtc cctggacac gcctgttccc cccgtgtacg 1080
ccgagaccaa gcacttcctc tacttcctag gcgcacaaggaa gcagctgcgg ccctccttcc 1140
tactcagtc tctgaggccc agcctgactg gcgcgcggag gctcgtggag accattttc 1200
tgggttccag gcccgttgc ccaaggactc cccgcagggtt gccccgcctg ccccaagcgct 1260
actggcaat gcccgttgc tttctggagc tgcttggaa ccacgcgcag tgcccctacg 1320
gggtgtctcc caagacgcac tgccgcgtc gagctgcggt caccgcac gcccgtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccgaa ggaggaggac acagaccccc 1440
gtcgccgttgc gcaagctgcgc cgcgcgcaca gcagccccgt gcaagggttac ggcttcgtgc 1500
gggcgtgcct gcccgttgc gtcggcccgat gcctctgggg ctccaggac aacgaacgcc 1560
gttccctca gaaacccaag aagtccatc ccctggggaa gcatgcac gtcgcgtgc 1620
agagacgtac gtggaaatg agcgtgcggg actgcgcctt gctgcgcagg agcccagggg 1680
ttggctgtgt tccggccgc gaggcaccgtc tgctgtggaa gatcctggcc aagttccgtc 1740
actggctgtat gagggtgtac gtcgcgtgc gtcgcgtgc tttctttat gtcacggaga 1800

ccacgttca aaagaacagg ctctttctt accggaagag tgcgtggagc aagttgcaaa 1860
 gcattggaat nnngacagtc accagggggg ttgaccgccc gactgggcgt ccccaagggtt 1920
 gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
 tgcgtgggt ggacgtggcc cccggcatgg ccttctgcgt gtgcgtggcgt gggtgccctg 2040
 agccctcaact gagtcgggtgg gggcttggcgtt cttccctgtga gcttccccctt agtctgttgt 2100
 ctggctgagc aaggcctcctg aggggctctc tattg 2135

<210> 52
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> N-Terminal Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala

210	215	220													
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
225						230			235					240	
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
					245			250					255		
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
					260			265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
					275			280				285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
					290			295			300				
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
					305			310			315			320	
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
					325			330				335			
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
					340			345				350			
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
					355			360			365				
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
					370			375			380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
					385			390			395			400	
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
					405			410				415			
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
					420			425				430			
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
					435			440			445				
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
					450			455			460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
					465			470			475			480	
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
					485			490				495			
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp
					500			505				510			
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe

515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		
545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala		
565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg		
580	585	590
Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe		
595	600	605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly		
610	615	620

<210> 53
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Splicing Variant of Human Telomerase encoded by
 Intron Y, ORF2, before the termination codon.
 SEQ ID NOS: 51,55,59,63,67,71,75,79,83 encode this
 fragment

<400> 53		
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser		
1	5	10
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly		
20	25	30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg		
35	40	45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro		
50	55	60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala		
65	70	75
Ser Gly Trp Gly		

<210> 54
 <211> 537
 <212> PRT
 <213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<400> 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
50 55 60Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
85 90 95Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser
165 170 175Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
225 230 235 240Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
245 250 255Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly
 530 535

<210> 55
 <211> 2145
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1 (ver.2); with Introns Y and 1

<400> 55
 atgcccgcgc ctccccgtg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgtgcgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtcag 120
 cgcggggacc cggcgcttt cccgcgcgtg gtggccagt gcctgggtg cgtccctgg 180
 gacgcacggc cgcggggccgc cgcggggccgc ttccgcagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttggggc gcgcgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gttcccccg caggtgtctt gcctgaagga gctggtgcc cgagtgtgc 360
 agaggctgtg cgagcgcggc gccaagaacg tgcggccctt cggcttcgcg ctgctggacg 420
 gggccgcgg gggccccccc gaggccttca ccaccagcg ggcgcagctac ctgccccaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtggggct gctgctgcgc cgcgtggcg 540
 acgacgtgtc gttcacctg ctggcgcgt gcgcgtctt tgcgtgggt gctcccaact 600
 gcccctacca ggtgtgcggg cccgcgtgtt accagctcg cgcgtccact caggccgc 660
 ccccgccaca cgctagtggc ccccgaaaggc gtctggatg cgaacgggc tggaaaccata 720
 ggcgtcaggga ggcggggc cccctggggc tgccagcccc ggtgcggagg aggcgcgggg 780
 gcagtgcgg cccgaatctg cccgttgcggc agaggcccac ggcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtctt gggccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctcttgg 960
 agggtgcgtc ctctggcactc cgcactccc acccatccgt gggccgcagg caccacgcgg 1020
 gccccccatc cacatcgccg ccaccacgtc cctggacac gcctgttcc cccgtgtacg 1080
 ccggagaccaa gcacttcctc tacttcctcg ggcacaaggc gcaagctgcgg ccctccttc 1140
 tactcagctc tctggggccc agcctgactg ggcgtcggag gtcgtggag accattttc 1200
 tgggttccag gcccgttgcg ccaggactc cccgcagggtt gcccgcctg cccagcgct 1260
 actggcaaat gcccgttgcg tttctggagc tgctggaa ccacgcgcag tgcccctacg 1320
 ggggtctctt caagacgcac tgcccgttc gagctgcggt ccccccac gcccgtgtct 1380
 gtgcccggga gaagccccag ggcgttgcgg cggcccccga ggaggaggac acagaccccc 1440
 gtcgcctgtt gcaactgcgc cccgcaggc gcaagccctg gcaagggtgtac ggcttcgtgc 1500
 gggcgttgcgt gcccgttgcg tgccggccag gccttgcgg gtcaggcgc aacaaacgcc 1560
 gcttcctca gaaacaccaag aagttcatct ccctggggaa gcatgcac gtcgcgtgc 1620
 agagagctgac gtggaaatggt agcgtgcggg actgcgttc gtcgtgcagg agcccagggg 1680
 tttctgtgt tccggccgc gggccgcgc tgcgtgagga gatcctggcc aagttctgc 1740
 actggctgtat gagggtgtac gtcgtgcgc tgctcagggtc tttctttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctcttttc accgaaaggag tgcgtggagc aagttcaaa 1860
 gcatggaaat cagacacgcac ttgaagaggc tgcgtgcgc ggagctgtcg gaagcagagg 1920
 tcaggcagca tcggaaagcc aggcccgcgc tgctgacgtc cagactccgc ttcatcccc 1980
 agcctgacgg gtcggcccg attgtgaaca tggactacgt cgtggagcc agaacgttcc 2040
 gcaagagaaaa gagggtggct gtcgtttgtt ttaacttcct ttttaaccag aagccgagcg 2100
 ttcacactcg agggtgaagg cactgttcaac tacga 2145

<210> 56
 <211> 704
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1 (ver.2); encoded by SEQ ID
 NO:55, with Y Intron ORF1

<400> 56
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu
 675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
 690 695 700

<210> 57

<211> 619

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2): encoded by SEQ ID
 NO:55, with Intron Y ORF2 after the termination
 codon

<400> 57

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu
 595 600 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly
 610 615

<210> 58
 <211> 704
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 1 (ver.2); encoded by SEQ ID
 NO:55, with Intron Y ORF3

<400> 58
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

85	90	95
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys		
100	105	110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys		
115	120	125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly		
130	135	140
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr		
145	150	155
160		
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg		
165	170	175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu		
180	185	190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro		
195	200	205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala		
210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser		
225	230	235
240		
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg		
245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro		
260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly		
275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		
305	310	315
320		
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln		
325	330	335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp		
340	345	350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser		
355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		

385	390	395	400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu			
405	410	415	
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly			
420	425	430	
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro			
435	440	445	
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys			
450	455	460	
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg			
465	470	475	480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr			
485	490	495	
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp			
500	505	510	
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe			
515	520	525	
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp			
530	535	540	
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val			
545	550	555	560
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala			
565	570	575	
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg			
580	585	590	
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe			
595	600	605	
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			
610	615	620	
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val			
625	630	635	640
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg			
645	650	655	
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr			
660	665	670	
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu			
675	680	685	
Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly			

690

695

700

<210> 59
 <211> 2645
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2 (ver.2); with Intron Y and
 Alpha

<400> 59
 atgccgcgc ctcccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgtgcgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtcag 120
 cgcggggacc cggcgcttt cgcgcgcgtg gtggcccaagt gcctgggtgt cgtgcgc 180
 gacgcacggc cgcggggccgc cgcggggccgc ttccgcagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttggggc gcgcgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gttcccccgg caggtgtcct gcctgaagga gctggtgcc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgtggacg 420
 gggccgcgg gggcccccgg gaggccttca ccaccagcgt gcgcagctac ctgccaaca 480
 cggtgaccga cgcactgcgg gggagcgggg cgtggggct gctgctgcgc cgcgtggcg 540
 acgacgtgt ggttacactg ctggcactgcg gcgcgtctt tgcgtgt gctccagct 600
 ggccttacca ggtgtgcggg cgcgcgtgt accagctcg cgcgcact caggccgc 660
 ccccgccaca cgctagtggc ccccgaaaggc gtctggatg cgaacgggc tggaaaccata 720
 ggcgtcaggga ggcgggggtc cccctggggc tgccagcccc ggtgtcgagg aggcgcggg 780
 gcaatgcggc cgcgaatctg cgcgttgcggc agaggcccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtctt gggccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctttgg 960
 agggtgcgt ctctggcactcgc cgcactccc acccatccgt gggccgcag caccacgcgg 1020
 gccccccatc cacatgcgg ccaccacgtc cctggacac gcctgtccc cgggtgtacg 1080
 ccgagaccaa gcacttcctc tacttcctc tag gcgacaaggc gcagctgcgg ccctccttc 1140
 tactcagctc tctgaggccc agcctgactg gcgcgcggag gctcgtggag accattttc 1200
 tgggttccag gcccgttggatg ccaggactc cccgcagggtt gccccgcctg cccagcgct 1260
 actggcaaat gcccgttggatg tttctggagc tgctggaa ccacgcgcag tgcccctacg 1320
 ggggtcttccat caagacgcac tgccgcgtc gagctgcggt caccgcgcac gcccgtgtct 1380
 gtgcggggaa gaagccccag ggtctgtgg cggccccggc ggaggaggac acagaccccc 1440
 gtcgcctgtt gcaatgcgtc cgcgcggcaca gcagccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct ggcggggctg gtgcggggcag gcctctgggg ctccaggac aacgaacgac 1560
 gcttcctca gaaacaccaag aagttcatct ccctggggaa gcatgcacgc ctctcgctgc 1620
 agagagctgac gtggaaagatg agcgtgcggg actgcgttgc gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgcgca gaggcaccgtc tgctgtggaa gatcctggcc aagttctgc 1740
 actggctgtat gagggtgtac gtcgtgcggc tgctcagggtc tttttttt gtcacggaga 1800
 ccacgtttca aaagaacagg ctcttttct accgcacgc gtcgtggagc aagttgcaaa 1860
 gcatggaaat cagacacgcac ttgaagaggc tgcaatgcgtc ggagctgtcg gaagcaggagg 1920
 tcaggcgcgc tggggaaagcc aggccccccc tgctgcgtc cagactccgc ttcatcccc 1980
 agcctgacgg gtcggggccg attgtgaaca tggactacgt cgtggagcc agaacgttcc 2040
 gcagagaaaa gaggcccggc gtcgttccact cgagggtgaa ggcactgttc agcgtgtca 2100
 actacgagcg ggcgcggcgc cccggccccc tgggcgcctc tgcgtgtggc ctggacgata 2160
 tccacaggcc ctggcgcacc ttcgtgtgc gtcgtgcggc ccaggacccg cgcctgagc 2220
 tgcgttgcgtt caagggtggat gtgcggggc gtcgttccact cttccatccat gacaggctca 2280
 cggagggtcat cgcgcgcgcgc atcaaaccccc agaacacgtt ctgcgtgcgt cggatgcgg 2340
 tgggtccagaa ggcggcccat gggcactgtcc gcaaggccctt caagagccac gtcctacgtc 2400
 cagtgccagg gatccgcgc gggctccatc ctctccacgc tgctctgcag cctgtgtac 2460

ggcgacatgg agaacaagct gtttgcgggg attcggcgaa acgggctgct cctgcgtttg 2520
 gtggatgatt tcttgttggt gacacctcac ctcacccacg cggaaacctt cctcaggacc 2580
 ctggtccgag gtgtccctga gtatggctgc gtggtaact tgcgaaagac agtggtaac 2640
 ttccc 2645

<210> 60
 <211> 841
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2 (ver.2); encoded by SEQ ID
 NO:59, with Intron Y ORF1

<400> 60
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg
465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro
 785 790 795 800

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln
 805 810 815

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala
 820 825 830

Gly Arg Ala Ala Pro Ala Phe Val Gly
835 840

<210> 61
<211> 756
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
NO:59 with Intron Y ORF2 after the termination
codon

<400> 61
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro Glu Ala Phe
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val Gly Asp Asp
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380

Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700

Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro
 705 710 715 720

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
 725 730 735

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
 740 745 750

Ala Phe Val Gly
 755

<210> 62
 <211> 841
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:
 59 with Intron Y ORF3

<400> 62
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

1	5	10	15												
His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
				20				25						30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg
				35			40						45		
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro
				50			55				60				
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Pro	Pro	Arg	Gly	Arg	Arg
						65			70		75			80	
Pro	Ala	Gly	Val	Glu	Gly	Gly	Arg	Gly	Glu	Pro	Ala	Thr	Cys	Gly	Glu
				85				90					95		
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys
				100				105					110		
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
				115			120				125				
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly
						130			135			140			
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr
						145			150		155			160	
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Arg	
				165				170					175		
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu
						180			185					190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
							195			200			205		
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
						210			215			220			
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
						225			230		235			240	
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
						245			250				255		
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
							260			265			270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
						275			280			285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
						290			295			300			
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu

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Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln			
325	330	335	
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp			
340	345	350	
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser			
355	360	365	
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu			
370	375	380	
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu			
385	390	395	400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu			
405	410	415	
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly			
420	425	430	
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro			
435	440	445	
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys			
450	455	460	
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg			
465	470	475	480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr			
485	490	495	
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp			
500	505	510	
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe			
515	520	525	
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp			
530	535	540	
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val			
545	550	555	560
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala			
565	570	575	
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg			
580	585	590	
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe			
595	600	605	
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			

610	615	620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val		
625	630	635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg		
645	650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr		
660	665	670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu		
675	680	685
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala		
690	695	700
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile		
705	710	715
720		
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro		
725	730	735
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp		
740	745	750
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys		
755	760	765
Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala		
770	775	780
Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro		
785	790	795
800		
Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln		
805	810	815
Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala		
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Gly Arg Ala Ala Pro Ala Phe Val Gly		
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and Beta		
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<220>
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 with Intron Y ORF1

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 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro		
260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly		
275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
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Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		
305	310	315
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln		
325	330	335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp		
340	345	350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser		
355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
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Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		

545	550	555	560
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala			
565	570	575	
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg			
580	585	590	
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe			
595	600	605	
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			
610	615	620	
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val			
625	630	635	640
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg			
645	650	655	
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr			
660	665	670	
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu			
675	680	685	
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala			
690	695	700	
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile			
705	710	715	720
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro			
725	730	735	
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp			
740	745	750	
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys			
755	760	765	
Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala			
770	775	780	
Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu			
785	790	795	800
Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu			
805	810	815	
Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu			
820	825	830	
Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys			
835	840	845	
His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly			

850	855	860
Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr		
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Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu		
885	890	895
Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr		
900	905	910
His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr		
915	920	925
Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu		
930	935	940
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly		
945	950	955
960		
Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val		
965	970	975
Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu		
980	985	990
Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu		
995	1000	1005
Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln		
1010	1015	1020
Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu		
1025	1030	1035
1040		
Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His		
1045	1050	1055
Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp		
1060	1065	1070
Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser		
1075	1080	1085
Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln		
1090	1095	1100
Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val		
1105	1110	1115
1120		
Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu		
1125	1130	1135
Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala		
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Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp		

1155

1160

1165

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 <211> 1081
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 with Intron Y ORF2 after the termination codon

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 35 40 45
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro Glu Ala Phe
 50 55 60
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
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 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys
 995 1000 1005
 Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His
 1010 1015 1020
 Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro
 1025 1030 1035 1040
 Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu
 1045 1050 1055
 Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Asn Pro Ala Leu
 1060 1065 1070
 Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1075 1080

<210> 66
 <211> 1165
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF3

<400> 66

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80

Pro Ala Gly Val Glu Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070
 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 1075 1080 1085
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 1090 1095 1100
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1105 1110 1115 1120
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1125 1130 1135
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1140 1145 1150
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1155 1160 1165

<210> 67
 <211> 3173
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein (ver.2); with Introns Y, Alpha,
 Beta and 2

<400> 67

atgccgcgcg ctccccgtg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
 gtgtgcgcg tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtcgag 120
 cgcggggacc cggcgcttt ccgcgcgtg gtggccca gcttgcgtgt cgtgcctgg 180
 gacgcacggc cggccccccgc cggccccctcc ttccgcagg tgggcctccc cggggtcggc 240
 gtccggctgg gttttagggc gcgcgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gttccccccg caggtgtctt gcctgaagga gctggtgcc cgagtgtgc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggctt cggcttcgcg ctgctggacg 420
 gggccgcgg gggccccccc gaggccttca ccaccagcgt ggcgcagctac ctgccccaa 480
 cggtgaccga cgcactgcgg gggagcgggg cgtggggct gctgctgcgc cgcgtggcg 540
 acgacgtgtc gttcacctg ctggcacgt gcgcgtctt tgcgtgtgt gctccca gcttccagct 600
 ggcgcctacca ggtgtgcggg cgcgcgtgt accagctcg cgcgcact caggccgc 660
 ccccgccaca cgcgtatggc cccgcgaaggc gtctggatg cgaacggggc tggaaaccata 720
 gcgtcaggga gcccgggtc cccctggcc tgccagcccc gggtgcgagg aggcgcggg 780
 gcaagtccag ccgaagtctg cgcgttccca agagggccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtctt gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg ttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc accttttg 960
 agggtgcgtc ctctggcacg cgcactccc acccatccgt gggccgcag caccacgcgg 1020
 gccccccatc cacatgcgg ccaccacgtc cctggacac gcctgttcc ccggtgtacg 1080
 ccgagaccaa gcacttcctc tacttcctcg gcgcacaaggc gcagctgcgg ccctccttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgcgtggag gctcgtggag accattttc 1200
 tgggttccag gcccgttggatg ccaggactc cccgcagggtt gcccgcctg cccagcgct 1260
 actggcaaat gcccgttggatg ttctgtgtc tgcttggaa ccacgcgcag tgcccctacg 1320
 gggtgcgtctt caagacgcac tgccgcgtc gagtgcgtt caccgcgcac gcccgtgtct 1380
 gtgcggggaa gaagccccag ggcgttggc cggcccccga ggaggaggac acagacccc 1440
 gtcgcctggt gcagctgcgc cgcgcacca gcagccccgt gcaagggttgc ggcttcgtgc 1500
 gggcgtgcct ggcgcggctg gtgcggggccag gcctctgggg ctccaggac aacgaacgc 1560
 gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgcaccc accttcgtgc 1620
 agagagctgac gtggaaagatg agcgtgcggg actgcgcctt gtcgcgcagg agcccagg 1680
 ttggctgtgt tccggccgca gaggccgcgc tgcgtgagga gatcctggcc aagttcttc 1740
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 ccacgtttca aaagaacagg ctcttttcc accgaaaggag tgcgtgttgc aagttgcaaa 1860
 gcatggaaat cagacacgcac tgcgtgttgc ggcgcgttgc ggagctgtcg gaagcagagg 1920
 tcaggcagca tcggaaagcc aggccccccc tgctgacgtc cagactccgc ttcatcccc 1980
 agcctgacgg gtcgcggccg attgtgaaca tggactacgt cgtggagcc agaacgttcc 2040
 gcagagaaaa gaggccgcag cgtctcaccc cgggggtgaa ggcactgttc agcgtgtca 2100
 actacgagcc ggcgcggccgc cccggccccc tgggcgcctc tgcgtgttgc ctggacgata 2160
 tccacagggc ctggcgacc ttcgtgtc tggtgcgggc ccaggaccgc cgcctgagc 2220
 tgcgtgttgc caagggttgc tgacggggcg cgtacgcacac catccccccag gacaggctca 2280
 cggagggtcat cgcgcacccat atcaaaccccc agaacacgtt tgcgtgcgt cggatgcgc 2340
 tggtcagaa ggcgcggccat gggcacgttcc gcaaggccctt caagagccac gtcttaccc 2400
 tgacagaccc ccagccgtac atgcgcacgt tgcgtgtca cctgcaggag accagccgc 2460
 tgagggtatc cgtgcgtatc gagcagagct cctccctgaa tgaggccgc agtggctct 2520
 tgcacgttcc ctcacgttcc atgtgcccacc acgcgtgcgc catcaggggc aagttctacg 2580
 tccagtgcca gggatcccc cagggtctca tcctctccac gtcgtgtc agcctgtgt 2640
 acggcgacat ggagaacaag ctgtttcgcc ggattcgccg ggacgggttgc ctcctgcgtt 2700
 tggtggatga ttctgtgttgc tgacacccctt acctccacca cgcgaaaacc ttcttcagga 2760
 ccctgggtccg aggtgtccctt gatgtatggct ggcgtgttgc cttgcggaa acagtggta 2820
 acttccctgtt agaagacgag gcccgtgggtt gcaaggccctt tgcgtgttgc agcctgtgt 2880
 gcctattccc ctggcgccgc ctgcgtgttgc ataccggac cctggagggtt cagagcgact 2940
 actccaggtt agcgcacccgtt gcccggaaatg gacccgttgc cccgcgtgggg cagggtgtgc 3000
 tgcaggccgc ttgcgtccac ctctgttcc tgcgtggggca ggcgcactgccc aatccaaag 3060
 gtcagatgc cacagggttgc ccctcgccca atctggggctt gacccaaat gcatcttct 3120
 gtgggagtgat gggtgcctca caacgggagc agtttctgt gctatccat 3173

<210> 68

<211> 982
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF1

<400> 68
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975

Gln Ser Asp Tyr Ser Arg
 980

<210> 69
 <211> 897
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF2 after the termination
 codon

<400> 69
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880

Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895

Arg

<210> 70
 <211> 982
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein 3 (Ver.2); encoded by SEQ ID
 NO:67 with Intron Y ORF3

<400> 70
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

50	55	60	
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg			
65	70	75	80
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu			
85	90	95	
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys			
100	105	110	
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys			
115	120	125	
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly			
130	135	140	
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr			
145	150	155	160
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg			
165	170	175	
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu			
180	185	190	
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro			
195	200	205	
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala			
210	215	220	
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser			
225	230	235	240
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg			
245	250	255	
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro			
260	265	270	
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly			
275	280	285	
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe			
290	295	300	
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu			
305	310	315	320
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln			
325	330	335	
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp			
340	345	350	
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser			

355	360	365	
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu			
370	375	380	
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu			
385	390	395	400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu			
405	410	415	
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly			
420	425	430	
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro			
435	440	445	
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys			
450	455	460	
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg			
465	470	475	480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr			
485	490	495	
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp			
500	505	510	
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe			
515	520	525	
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp			
530	535	540	
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val			
545	550	555	560
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala			
565	570	575	
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg			
580	585	590	
Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe			
595	600	605	
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			
610	615	620	
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val			
625	630	635	640
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg			
645	650	655	
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr			

660	665	670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu		
675	680	685
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala		
690	695	700
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile		
705	710	715
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro		
725	730	735
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp		
740	745	750
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys		
755	760	765
Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala		
770	775	780
Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu		
785	790	795
Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu		
805	810	815
Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu		
820	825	830
Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys		
835	840	845
His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly		
850	855	860
Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr		
865	870	875
Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu		
885	890	895
Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr		
900	905	910
His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr		
915	920	925
Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu		
930	935	940
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly		
945	950	955
Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val		

965

970

975

Gln Ser Asp Tyr Ser Arg
980

<210> 71

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); with Introns
Y, Alpha, Beta and 3

<400> 71

atgcgcgcgc ctccccgtc ccgagccgtc cgctccctgc tgccgcggcc ctaccgcgag 60
 gtgctgcgcg tggccacgtt cgtgcggcgc ctggggccccc agggctggcg gctgggtgcag 120
 cgcggggacc cggcgcttt cccgcgcgtc gtggcccaagt gcctgggtgt cgtgcgcctgg 180
 gacgcacggc cgcgcgcgc cgcgcgcgtc ttccgcagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttggggc ggccgggggg aaccagcgcac atgcggagag cagcgcaggc 300
 gactcaggcgc gttcccccg cagggtgtct gcctgaagga gctggtgccc cgagtgcgtc 360
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgcgtggacg 420
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
 cgtgtacccgc cgcactgcgg gggagcgggg cgtggggct gctgctgcgc cgcgtggcg 540
 acgacgtgt ggttccacccgc ctggcgcacgt gcgcgcgtt tgcgtgggt gctcccaagct 600
 gcgccttacca ggtgtcgccc cgcgcgtgtt accagctcg cgcgcactt caggcccgcc 660
 cccccccaca cgctagtggc ccccgaaaggc gtctggatg cgaacggggcc tggaaaccata 720
 gctgtacggg gggccgggtc cccctggggc tgccagcccc gggtgcgagg aggcgcgggg 780
 gcaagtgcac ccgaagtctg cctgtgcaca agaggcccag gctgtggcgct gcccctgagc 840
 cgagcgggac gcccgttggg cagggtgtct gggcccaccc gggcaggacgc cgtggaccga 900
 gtgaccgtgg tttctgtgt gttcacccgc ccagaccgc cgaagaagcc accttttgg 960
 aggtgcgtct ctctggcactc cgccactccc acccatccgt gggccgcac caccacgcgg 1020
 gccccccatc cacatgcgg ccaccacgtc cctgggacac gcctgtccc cgggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgacaaggc gcaagctgcgg ccctccccc 1140
 tactcagctc tctgaggccc agcctgactg gcgcgtcgag gctcgtggag accatcttc 1200
 tgggttccag gcccgttgc ccaggactc cccgcagggtt gccccgcctg ccccaagcgc 1260
 actggcaaat gggccctgt tttctggagc tgcttggaa ccacgcgcag tgcccctacg 1320
 ggtgtctctt caagacgcac tgcccgtgc gagctgcgtt caccgcac gcccgtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccca gggaggaggac acagaccccc 1440
 gtcgcctgtt gcagctgcgc cgcacgcaca gcagccctg gcaggtgtac ggctcgtgc 1500
 gggcctgcct ggcgggctg gtgccccca ggcctctgggg ctccaggac aacgaacgc 1560
 gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
 agagactgac gtggaaagatg agcgtgcggg actgcgcctt gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccca gaggccgcgc tgcgtgagga gatcctggcc aagttcctgc 1740
 actggctgtat gagggtgtac gtcgtgcgc tgctcagggtc ttttttttgcacggaga 1800
 ccacgtttca aaagaacagg ctcttttct accggaaagag tgcgtggagc aagttgcaaa 1860
 gcatttggat cagacacgc ttgaagaggc tgcaagctgcg ggagctgtcg gaagcagagg 1920
 tcaggcagca tcggaaagcc aggccccccc tgctgacgtc cagactccgc ttcatcccc 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtggagcc agaacgttcc 2040
 gcagagaaaa gaggcccggc cgtctcacct cgagggtgaa ggcactgttc agcgtgtca 2100
 actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgcgtggc ctggacgata 2160
 tccacagggc ctggcgcacc ttctgtgtc gttgtgcggc ccaggacccg cccgcctgagc 2220
 tgcgtttgtt caagggtggat gtgacggggc cgtacgacac catccccca gacaggctca 2280
 cgaggtcat cggccacatc atcaaaccccc agaacacgtt ctgcgtgcgt cggatgcgc 2340
 tgcgtccagaa ggccggccat gggcacgtcc gcaaggccctt caagagccac gtctctaccc 2400
 tgacagacccctt ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagccgc 2460

tgaggatgc cgtcgtcatc gaggcagact cctccctgaa tgaggccagc agtggcctct 2520
 tcgacgtctt cctacgcttc atgtgccacc acgcccgtgcg catcaggggc aagtccctacg 2580
 tccagtgcctt ggggatccc cagggctcca tcctctccac gctgctctgc agcctgtgt 2640
 acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt 2700
 tggatgtt tttcttgcgtt gtgacaccc acctcacccca cgcgaaaacc ttcctcaggaa 2760
 ccttgcgtcc aggtgtccct gaggatggct gctgtgtgaa cttgcggaaag acagtggta 2820
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 ctgggaggaa catgcgtcgc aaactctttt gggcttgcg gctgaagtgt cacagcctgt 3060
 ttctggattt gcaggtgaac agcctccaga cgggtgtcac caacatctac aagatcctcc 3120
 tgctgcaggc gtacaggttt cacgcgtgtt tgctgcgtt cccatttcat cagcaagttt 3180
 ggaagaacc cacattttt ctcgcgtca tctctgacac ggcctccctc tgctactcca 3240
 tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactctt gcggtgttg 3300
 ggtcgggaca gccagagatg gagccacccc gcagaccgtc ggggtgtggc agctttccgg 3360
 tgtctcctgg gaggggagtt gggctgggccc tgtgactctt cagcctctgt tttcccccaag 3420
 ggtatgtcgct gggggccaaag ggcgcgcggc gccccttgcc ctccga 3466

<210> 72

<211> 1130

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF1

<400> 72

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815

Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830

Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845

His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1125 1130

<210> 73

<211> 1045

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
 ID NO:71 with Intron Y ORF2 after the termination
 codon

<400> 73

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380

Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp
 660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr
 675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val
 690 695 700

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg
 725 730 735

Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser
 740 745 750

Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg
 755 760 765

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn
 785 790 795 800
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val
 805 810 815
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe
 820 825 830
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn
 835 840 845
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly
 850 855 860
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys
 865 870 875 880
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser
 885 890 895
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
 900 905 910
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg
 915 920 925
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln
 930 935 940
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg
 945 950 955 960
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys
 965 970 975
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys
 980 985 990
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Asn Ile Leu Val
 995 1000 1005
 Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro
 1010 1015 1020
 Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly
 1025 1030 1035 1040
 Val Gly Leu Gly Leu
 1045

<210> 74
 <211> 1130
 <212> PRT
 <213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
ID NO:71 with Intron Y ORF3

<400> 74

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
165 170 175Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
195 200 205Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
210 215 220Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
225 230 235 240Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
245 250 255Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp
 740 745 750
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
 755 760 765
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala
 770 775 780
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu
 785 790 795 800
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu
 805 810 815
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu
 820 825 830
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys
 835 840 845
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly
 850 855 860
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu
 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr
 915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly
 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val
 965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu
 980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu
 995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln
 1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu
 1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His
 1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp
 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu
 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro
 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val
 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1125 1130

<210> 75
 <211> 4022
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); with Introns Y
 and Beta

<400> 75

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 cgcggggacc cggcggttt cccgcgcgtg gtggcccaagt gcctgggtgtg cgtccccctgg 180
 gacgcacggc cgcgcgcgc cgcgcgcgc ttccggccagg tgggcctccc cggggtcggc 240
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 gacccaacat ctacaagatc ctccgtctgc aggctacag gtttgcacgc tgcgtgtgc 3120
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tcctgctcaa gctgactcga caccgtgtca cctacgtgcc actcctgggg tcactcagga 3360
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 cagccaaacc cggactgccc tcagacttca agaccatcct ggactgtatgg ccacccgccc 3480
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 tgcccgaggc ctgcattgtcc ggctgaaggc tgagtgtccg gctgaggcct gagcgagtgt 3660
 ccagccaagg gctgagtgcc cagcacaccc ggcgtttca cttccccaca ggctggcgct 3720
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 gaatagtcca tccccagatt cgccattgtt caccctcgc cctgcccctcc tttgccttc 3840
 acccccacca tccaggtgga gaccctgaga aggaccctgg gagctctgg aatttggagt 3900
 gaccaaagggt gtgcctgtta cacaggcag gaccctgcac ctggatgggg gtcctgtgg 3960
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 ga 4022

<210> 76

<211> 1154

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID NO:75 with Intron Y ORF1

<400> 76

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055
 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070
 Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro
 1075 1080 1085

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu
 1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr
 1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala
 1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile
 1140 1145 1150

Leu Asp

<210> 77
 <211> 1069
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF2 after the termination
 codon

<400> 77
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
 660 665 670
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
 675 680 685
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
 690 695 700
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
 705 710 715 720
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
 725 730 735
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
 740 745 750
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
 805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
 885 890 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
 900 905 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
 915 920 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
 930 935 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
 945 950 955 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
 965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
 980 985 990

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln
 995 1000 1005

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
 1010 1015 1020

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
 1025 1030 1035 1040

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala
 1045 1050 1055

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1060 1065

<210> 78
 <211> 1154
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
 NO:75 with Intron Y ORF3

<400> 78
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro		
260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly		
275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		
305	310	315
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln		
325	330	335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp		
340	345	350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser		
355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		

545	550	555	560
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala			
565	570	575	
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg			
580	585	590	
Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe			
595	600	605	
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			
610	615	620	
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val			
625	630	635	640
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg			
645	650	655	
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr			
660	665	670	
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu			
675	680	685	
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala			
690	695	700	
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile			
705	710	715	720
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro			
725	730	735	
Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala			
740	745	750	
Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val			
755	760	765	
Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His			
770	775	780	
Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala			
785	790	795	800
His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln			
805	810	815	
Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu			
820	825	830	
Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val			
835	840	845	
Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys			

850	855	860
Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg		
865	870	875
Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr		
885	890	895
Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly		
900	905	910
Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn		
915	920	925
Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met		
930	935	940
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg		
945	950	955
Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile		
965	970	975
Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met		
980	985	990
Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe		
995	1000	1005
Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr		
1010	1015	1020
Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln		
1025	1030	1035
Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg		
1045	1050	1055
Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys		
1060	1065	1070
Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro		
1075	1080	1085
Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu		
1090	1095	1100
Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr		
1105	1110	1115
Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala		
1125	1130	1135
Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile		
1140	1145	1150
Leu Asp		

<210> 79
 <211> 3137
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Truncated Protein Lacking Motif A (ver.2); with
 Introns Y, Beta and 2

<400> 79
 atgcccgcgc ctcccgctg ccgagccgtg cgctccctgc tgcgca gcca ctaccgcgag 60
 gtgtgcgc tggccacgtt cgtgcggcgc ctggggccccc agggctggcg gctgggtgcag 120
 cgcggggacc cggcggttt cgcgcgcgtg gtggcccagt gcctgggtgtg cgtgcctgg 180
 gacgcacggc cgcggcccccgc cgccccctcc ttccgcccagg tgggcctccc cggggtcggc 240
 gtccggctgg ggttggggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcaggc gcttcccccg cagggtgtcct gcctgaagga gctggtgcc cgagtgtgc 360
 agaggctgtg cgagcgcgc gcaagaacg tgctggcctt cggcttcgcg ctgtggacg 420
 gggcccgccg gggccccccc gaggccttca ccaccagcgt ggcgcagctac ctgcccaca 480
 cggtgacgcg cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtggcg 540
 acgacgtgt ggttccacctg ctggcacgt gcgcgcgtt tggctgggtg gctccca gct 600
 gcgcctacca ggtgtgcggg cgcgcgtgtt accagctcg cgcgcactt caggcccg 660
 cccccccaca cgcctagtggc ccccgaaaggc gtctggatg cgaacggggc tggaaaccata 720
 ggcgtcaggga ggccggggc cccctggggc tgccagcccc ggtgtcgagg agggcgggg 780
 gcaagtgcg cccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
 cggagcggac gcccgttggg caggggtctt gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgttg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc accttttg 960
 agggtgcgt ctctgcacg cgcactccc acccatccgt gggccgcac caccacgcgg 1020
 gccccccatc cacatgcgg ccaccacgtc cctggacac gcctgttcc cgggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgcacaaggc gcaagctgcgg ccctcttcc 1140
 tactcagctc tctgaggccc agcctgactg gcgcgcggag gctcgtggag accatcttc 1200
 tgggttccag gcccgttggatg ccaggactc cccgcagggtt gccccgcctg cccca gcgct 1260
 actggcaaat gcccgttggatg tttctggagc tgcttggaa ccacgcgcag tgcccctacg 1320
 ggtgtctctt caagacgcac tgcccgtgc gagctgcggcgt caccggcaca gcccgtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggccccca gggaggaggac acagacccc 1440
 gtcgcctgtt gcagctgcgc cgcgcgcaca gcagccccctg gcaggtgtac ggctcgtgc 1500
 gggcctgcct gcccgttggatg tttctggagc tgcttggaa ccacgcgcag aacgaacgc 1560
 gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgtgc 1620
 agagactgac gtggaaagatg agcgtgcggg actgcgcctt gctgcgcagg agcccagg 1680
 ttggctgtgt tccggccgca gaggccgc tgcgtgagga gatcctggcc aagtccctgc 1740
 actggctgtat gagtgtgtac gtcgtcgagc tgctcagggtc tttcttttgc acgtgcgtt 1800
 ccacgtttca aaagaacagg ctcttttgc accggaaaggat gtcgtggagc aagttgcaaa 1860
 gcatttggat cagacacgcac ttgaagaggc tgca gtcgcggcgt ggagctgtcg gaagcagg 1920
 tcaggcagca tcggaaaggcc aggccccccc tgctgacgtc cagactccgc ttcatcccc 1980
 agcctgacgg cgtgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
 gcagagaaaa gaggcccggag cgtctcacctt cgagggtgaa ggcactgttc agcgtgtca 2100
 actacgagcg ggcgcggcgc cccggccccc tgggcgcctc tgcgtggc ctggacgata 2160
 tccacaggc cttggccgacc ttctgtgtc tgcgtggc ccaggacccg cccgcctgagc 2220
 tgcgttgcgtt caaggacagg ctcacggagg tcatgcgcag catcatcaaa cccca gagaaca 2280
 cgtactgcgt ggcgtcggtat ggcgtggcc tggactacgt cgtgggagcc agaacgttcc 2340
 ccttcaggat ccacgtctt accttgcacat acctccagcc gtcacatgcgc gatcgtgtcc 2400
 ctcacactgcg ggagaccagg cgcgtggagg atgcgtcgat catgcgcagg agcgttccccc 2460
 tgaatgaggc cagcagtggc ctcttcgacg tcttcctacg ttcatgtgc caccacgcgg 2520
 tgcgcatcag gggcaagtcc tacgtccagt gccaggat cccgcaggc tccatcctct 2580
 ccacgctgtc ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640

ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
 cccacgcgaa aaccttcctc aggaccctgg tccgagggtgt ccctgagtat ggctgcgtgg 2760
 tgaacctgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
 ctttgttca gatgccggcc cacggcctat tcccctggc cgccctgcgt ctggatacc 2880
 ggaccctgga ggtgcagagc gactactcca ggtgagcgc a cttggccggaa agtggagcct 2940
 gtgcccggct ggggcagggtg ctgctgcagg gccgtgcgt ccacctctgc ttccgtgtgg 3000
 ggcaggcgc tgccaatccc aaagggtcag atgcccacagg gtgcccctcg tcccacatctgg 3060
 ggctgagcac aaatgcacatct ttctgtggga gtgagggtgc ctcacaacgg gagca gttt 3120
 ctgtgctatt ttggtaa 3137

<210> 80
 <211> 970
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF1

<400> 80
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

195	200	205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala		
210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser		
225	230	235
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg		
245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro		
260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly		
275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		
305	310	315
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln		
325	330	335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp		
340	345	350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser		
355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		

500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		
545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala		
565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg		
580	585	590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe		
595	600	605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg		
610	615	620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val		
625	630	635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg		
645	650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr		
660	665	670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu		
675	680	685
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala		
690	695	700
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile		
705	710	715
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro		
725	730	735
Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala		
740	745	750
Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val		
755	760	765
Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His		
770	775	780
Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala		
785	790	795
His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln		

805	810	815
Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu		
820	825	830
Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val		
835	840	845
Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys		
850	855	860
Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg		
865	870	875
Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr		
885	890	895
Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly		
900	905	910
Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn		
915	920	925
Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met		
930	935	940
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg		
945	950	955
Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg		
965	970	

<210> 81
 <211> 885
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF2 after the
 termination codon

<400> 81		
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr		
1	5	10
15		
Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg		
20	25	30
Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe		
35	40	45
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe		
50	55	60
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu		

65	70	75	80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp			
85		90	95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala			
100		105	110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly			
115	120	125	
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg			
130	135	140	
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly			
145	150	155	160
Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser			
165		170	175
Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala			
180		185	190
Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro			
195	200	205	
Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro			
210	215	220	
Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly			
225	230	235	240
Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro			
245		250	255
Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro			
260	265	270	
Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu			
275	280	285	
Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr			
290	295	300	
Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp			
305	310	315	320
Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp			
325		330	335
Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys			
340		345	350
Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val			
355	360	365	
Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val			

370	375	380	
Ala Ala Pro Glu Glu	Asp Thr Asp Pro Arg	Arg Leu Val Gln Leu	
385 390	395	400	
Leu Arg Gln His Ser Ser	Pro Trp Gln Val Tyr	Gly Phe Val Arg Ala	
405	410	415	
Cys Leu Arg Arg	Leu Val Pro Pro	Gly Leu Trp Gly Ser Arg His Asn	
420	425	430	
Glu Arg Arg Phe Leu Arg Asn	Thr Lys Lys Phe Ile Ser	Leu Gly Lys	
435	440	445	
His Ala Lys Leu Ser Leu	Gln Glu Leu Thr Trp	Lys Met Ser Val Arg	
450	455	460	
Asp Cys Ala Trp Leu Arg Arg	Ser Pro Gly Val Gly	Cys Val Pro Ala	
465	470	475	480
Ala Glu His Arg Leu Arg Glu Glu	Ile Leu Ala Lys Phe	Leu His Trp	
485	490	495	
Leu Met Ser Val Tyr Val Val	Glu Leu Leu Arg Ser	Phe Tyr Val	
500	505	510	
Thr Glu Thr Thr Phe Gln Lys	Asn Arg Leu Phe Phe	Tyr Arg Lys Ser	
515	520	525	
Val Trp Ser Lys Leu Gln Ser	Ile Gly Ile Arg Gln	His Leu Lys Arg	
530	535	540	
Val Gln Leu Arg Glu Leu Ser	Glu Ala Glu Val Arg	Gln His Arg Glu	
545	550	555	560
Ala Arg Pro Ala Leu Leu Thr Ser Arg	Leu Arg Phe Ile Pro	Lys Pro	
565	570	575	
Asp Gly Leu Arg Pro Ile Val Asn	Met Asp Tyr Val Val	Gly Ala Arg	
580	585	590	
Thr Phe Arg Arg Glu Lys Arg	Ala Glu Arg Leu Thr	Ser Arg Val Lys	
595	600	605	
Ala Leu Phe Ser Val Leu Asn	Tyr Glu Arg Ala Arg	Arg Pro Gly Leu	
610	615	620	
Leu Gly Ala Ser Val Leu	Gly Leu Asp Asp	Ile His Arg Ala Trp Arg	
625	630	635	640
Thr Phe Val Leu Arg Val Arg	Ala Gln Asp Pro Pro	Pro Glu Leu Tyr	
645	650	655	
Phe Val Lys Asp Arg Leu Thr	Glu Val Ile Ala Ser	Ile Lys Pro	
660	665	670	
Gln Asn Thr Tyr Cys Val Arg	Arg Tyr Ala Val Val	Gln Lys Ala Ala	

675	680	685
His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr		
690	695	700
Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr		
705	710	715
720		
Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn		
725	730	735
Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His		
740	745	750
His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile		
755	760	765
Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly		
770	775	780
Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu		
785	790	795
800		
Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His		
805	810	815
Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly		
820	825	830
Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp		
835	840	845
Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu		
850	855	860
Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln		
865	870	875
880		
Ser Asp Tyr Ser Arg		
885		

<210> 82
 <211> 970
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Protein lacking Motif A (ver.2); encoded
 by SEQ ID NO:79 with Intron Y ORF3

<400> 82
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 65 70 75 80

Pro Ala Gly Val Glu Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
 85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
 965 970

<210> 83
 <211> 3432
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); with Intron Y, Beta and 3

<400> 83
 atgcccgcgc ctccccgtc ccgagccgtc cgctccctgc tgcgcagccca ctaccgcgag 60
 gtgctgccgc tggccacgtt cgtgcggcgc ctggggccccc agggctggcg gctgggtcgag 120
 cgcggggacc cggcggttt cccgcgcgtc gtggcccaagt gcctgggtgtc cgtgcccgtt 180
 gacgcacggc cgcggccgc cgcggccgtt ttccggccagg tgggcctccc cggggtcggc 240
 gtcggctgg ggttgagggc ggccgggggg aaccacgcac atgcggagag cagcgcaggc 300
 gactcaggc gcttcccccg cagggtgtcct gcctgaagga gctggtgccc cgagtgtgc 360
 agaggctgtg cggcgccgc gcaagaacg tgctggcctt cggcttcggc ctgctggacg 420
 gggccgcgg gggcccccgg gaggccttca ccaccacgtc ggcgcagctac ctgccccaca 480
 cgtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtggcg 540
 acgacgtgt ggttcacctg ctggcacgtc gcgcgtctt tggctgggtg gctcccaact 600
 ggcctacca ggtgtcgccc cgcggcgtgt accagctgg cgtgcact caggccggc 660
 ccccgcaca cgttagtggc cccgcaggc gtctggatg cgaacggggc tggaccata 720
 gcgtcaggga ggccggggtc cccctggccc tgccagcccc ggggtgcgagg agggcgggg 780
 gcagtgcac cccaagtctg ccgttgcaca agaggcccag gcgtggcgct gcccctgagc 840
 cgagcggac gcccgttggg caggggcctt gggcccaccc gggcaggacg cgtggaccga 900
 gtgaccgtgg tttctgtgt gtgtcacctg ccagacccgc cgaagaaggc accttttgg 960
 agggtcgtct ctctggcacg cgccactccc acccatccgt gggccgcac caccacgcgg 1020
 gccccccatc cacatgcgg ccaccacgtc cctgggacac gccttgcctt ccgggtgtacg 1080
 ccgagaccaa gcaacttcctc tactcctcag gcgacaagga gcagctgcgg ccctcccttc 1140
 tactcgtctc tctgaggccc agcctgactg ggcgtcgagg gtcgtggag accatcttc 1200
 tgggttccag gcccgttgc ccaaggactc cccgcagggtt gccccgcctt ccccaacgcgt 1260
 actggcaaat gcccgttgc tttctggagc tgcttggaa ccacgcgcac tgcccttacg 1320
 ggtgtctctt caagacgcac tgcccgtgc gagctgcgtt caccacggca gccgtgtct 1380
 gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440
 gtcgcctggt gcaagctgtc cgccacgcaca gcagccccgt gcaagggttac ggctcgtgc 1500
 gggcctgcct gcccgttgc tttctggagc gccttgggg ctccaggcac aacaaacgc 1560
 gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgtgc 1620
 agagactgac gtggaaagatg agcgtcgagg actgcgtt gtcgtcgagg agccagggg 1680
 ttggctgtgt tccggccca gacccgtc tgcgtgagga gatcctggcc aagttccgtc 1740
 actggctgtat gagtgtgtac gtcgtcgagc tgctcagggtc tttctttat gtcacggaga 1800
 ccacgtttca aaagaacagg ctcttttcc accggaaagag tgcgtggagc aagttgcaaa 1860
 gcatttggat cagacacgcac ttgaagagg tgcgtcgcc ggagctgtcg gaagcagg 1920
 tcaggcagca tcgggaagcc aggccccccc tgctgacgtc cagactccgc ttcatcccc 1980
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtggggagcc agaacgttcc 2040
 gcagagaaaa gaggcccggc cgtctcaccc cgagggtgaa ggcactgttc agcgtgtca 2100
 actacgagcg ggcggccgc cccggccccc tggggccccc tgcgtggcc ctggacgata 2160
 tccacaggcc ctggcgacc ttctgtgtc gtgtgcggcc ccaggacccc cgcctgagc 2220
 tgcgtttgtt caaggacagg ctcacggagg tgcgtcgccag catcatcaaa ccccaagaaca 2280
 cgtactgcgt gcaagggtat gcccgttgc ccatggccac gtccgcaagg 2340

ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
 ctcacactgca ggagaccagc ccgctgaggg atgcccgtcg catcgagcag agctccccc 2460
 tgaatgaggg cagcagtggc ctcttcgacg tcttcctacg cttcatgtgc caccacgccc 2520
 tgcgcatca gggcaagtcc tacgtccagt gccagggat cccgcagggc tccatcctct 2580
 ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
 ggcgggacgg gtcgtccctg ctgtttgggg atgatttctt gttggtgaca cctcacctca 2700
 cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagttat ggctgcgtgg 2760
 tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
 cttttgtca gatgcggcc cacggccat tcccctgggtg cggcctgctg ctggatacc 2880
 ggaccctgga ggtcagagc gactactcca gctatgccc gacctccatc agagccagtc 2940
 tcacattcaa ccgcgcgttc aaggctggg ggaacatgcg tcgcaaactc tttgggtct 3000
 tgcggctgaa gtgtcacagc ctgtttctgg atttgcaggt gaacagccctc cagacgggt 3060
 gcaccaacat ctacaagatc ctcctgctc aggcgtacag gtttcacgca tgtgtgctgc 3120
 agtccccatt tcatcagcaa gtttggaaaga accccacatt tttcctgcgc gtcatctctg 3180
 acacggccctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
 ctgtcggtac ccctcggtg cttgggtcgg gacagccaga gatggagcca ccccgccagac 3300
 cgtcgggtgt gggcagctt ccgggtgtctc ctgggggggg agttgggtctg ggcctgtgac 3360
 tcctcagccct ctgtttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
 tgccctccga ga 3432

<210> 84

<211> 1122

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF1

<400> 84

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145 150 155 160
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165 170 175
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180 185 190
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195 200 205
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210 215 220
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225 230 235 240
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 275 280 285
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe
 290 295 300
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 305 310 315 320
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 325 330 335
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp
 340 345 350
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser
 355 360 365
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu
 370 375 380
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu
 385 390 395 400
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu
 405 410 415
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
 420 425 430
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
 450 455 460
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg
 465 470 475 480
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
 485 490 495
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
 500 505 510
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
 515 520 525
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
 530 535 540
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
 545 550 555 560
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
 565 570 575
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
 580 585 590
 Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe
 595 600 605
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg
 610 615 620
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val
 625 630 635 640
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg
 645 650 655
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr
 660 665 670
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu
 675 680 685
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala
 690 695 700
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile
 705 710 715 720
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro
 725 730 735
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala
 740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 755 760 765

Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His
 770 775 780

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
 785 790 795 800

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
 805 810 815

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
 820 825 830

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val
 835 840 845

Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys
 850 855 860

Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg
 865 870 875 880

Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
 885 890 895

Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly
 900 905 910

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn
 915 920 925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile
 965 970 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met
 980 985 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe
 995 1000 1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr
 1010 1015 1020

Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln
 1025 1030 1035 1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
 1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys
 1060 1065 1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
 1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile
 1105 1110 1115 1120

Gly Ala

<210> 85

<211> 1037

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF2 after the termination codon

<400> 85

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser
 165 170 175
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala
 180 185 190
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro
 195 200 205
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro
 210 215 220
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly
 225 230 235 240
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro
 245 250 255
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro
 260 265 270
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu
 275 280 285
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr
 290 295 300
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp
 305 310 315 320
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp
 325 330 335
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys
 340 345 350
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val
 355 360 365
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val
 370 375 380
 Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu
 385 390 395 400
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala
 405 410 415
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn
 420 425 430
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
 435 440 445
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys
 595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu
 610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg
 625 630 635 640

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr
 645 650 655

Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro
 660 665 670

Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala
 675 680 685

His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr
 690 695 700

Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr
 705 710 715 720

Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn
 725 730 735

Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His
 740 745 750

His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
 770 775 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu
 785 790 795 800

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His
 805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly
 820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
 835 840 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 850 855 860

Phe Pro Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
 865 870 875 880

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
 885 890 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
 900 905 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
 915 920 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
 930 935 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
 945 950 955 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
 965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu
 980 985 990

Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu
 995 1000 1005

Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser
 1010 1015 1020

Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala
 1025 1030 1035

<210> 86

<211> 1122

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
(ver.2); encoded by SEQ ID NO:83 with Intron Y
ORF3

<400> 86

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
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<220>
 <223> Description of Unknown Organism: Consensus P-loop
 Motif Sequence found in large number of protein
 families

<220>
 <221> MOD_RES
 <222> (2)..(5)
 <223> Wherein Xaa is any residue

<400> 91
 Ala Xaa Xaa Xaa Xaa Gly Lys Ser
 1 5

<210> 92
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 92
 Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Cys Val
 1 5 10 15

Gly

<210> 93
 <211> 9
 <212> PRT
 <213> Unknown

<220>
<223> Description of Unknown Organism: Consensus c-Alb
SH3 binding peptide

<220>
<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

<220>
<221> MOD_RES
<222> (7)..(8)
<223> Wherein Xaa is any residue

<400> 93
Pro Xaa Xaa Xaa Xaa Pro Xaa Xaa Pro
1 5

<210> 94
<211> 17
<212> PRT
<213> Homo sapiens

<400> 94
His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr
1 5 10 15
Pro

<210> 95
<211> 14
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: General Target
Sequence Recognized by Hairpin Ribozyme

<220>
<221> modified_base
<222> (1)..(3)
<223> Wherein N is G, U, C or A

<220>
<221> modified_base
<222> (5)
<223> Wherein N is G, U, C or A

<220>
<221> modified_base
<222> (9)..(14)
<223> Wherein N is G, U, C or A

<400> 95
nnnbngucnn nnnn 14

<210> 96
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

<400> 96
aggagatctc gcgatgccgc gcgctc 26

<210> 97
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

<400> 97
tccacgcgtc ctgcccgggt g 21

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

<400> 98
gctggtgca g cgcggggacc 20

<210> 99
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amplification
Primer Design Based on EST Sequence GenBank
Accession Number AA281296

<400> 99
cacaagctt aattcacatc tcaccatgaa ggagctggtg gcccggat 48

<210> 100
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 100
ggcacgcaca ccaggcactg 20

<210> 101
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 101
cctgcctgaa ggagctgg 20

<210> 102
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 102
ggacacacctgg cggaaggag 19

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 103
ccgagtgctg cagaggctgt 20

<210> 104
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized

Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 104
gaagccgaag gccagcacgt tctt 24

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 105
gtgcagctgc tccgcccagca ca 22

<210> 106
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 106
gttcccaaggc agctccagaa acag 24

<210> 107
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 107
ggcagtgcgt cttgaggaggc a 21

<210> 108
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 108
cactggctga tgagtgtgt a 21

<210> 109
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 109
gacgtacaca ctcatcagcc ag 22

<210> 110
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 110
ggctttctt ttatgtcacg gag 23

<210> 111
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 111
cacttgaaga gggtgagct 20

<210> 112
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 112
gtctcaccc gagggtgaag 20

<210> 113
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 113
ttcacccctcg aggtgagacg ct

22

<210> 114
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 114
tcgtagttga gcacgctgaa c

21

<210> 115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 115
gcctgagctg tactttgtca a

21

<210> 116
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 116
ctgagctgta ctttgtcaag gaca

24

<210> 117
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 117
gtacatgcga cagttcgtgg ctca 24

<210> 118
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 118
catgaagcgt aggaagacgt cgaaga 26

<210> 119
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 119
cgcaaacagc ttgttctcca tgtc 24

<210> 120
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 120
ctatccccgg acctccatca ga 22

<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 121
ctgatggagg tccggggata g 21

<210> 122

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 122
cctccgaggc cgtgcagt 18

<210> 123
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 123
cacctaaggc tttcttagatc agtccaggat ggtcttgaag tca 43

<210> 124
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 124
ggaaggcaaa ggagggcagg gcga 24

<210> 125
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 125
cacgaattcg gatccaaagct tttttttt tttttt 37

<210> 126
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 126

gggttgcggga ggggtgggc

18

<210> 127

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 127

gcagtggta gccgagtcct g

21

<210> 128

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 128

cgactttgga ggtgccttca

20

<210> 129

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 129

gctgggtgcag cgcggggacc

20

<210> 130

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 130

gaggtgcaga gcgactactc ca 22
<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 131
gtctcacctc gagggtaag 20

<210> 132
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 132
ggctgctcct gcgttggtg ga 22

<210> 133
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 133
gccagagatg gagccaccc 19

<210> 134
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 134
gggtggctcc atctctggc 19

<210> 135
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 135
ccgcacgctc atcttccacg t 21

<210> 136
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 136
gcttgggat gaagcggtc 19

<210> 137
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 137
cgcctgagct gtactttgtc a 21

<210> 138
<211> 46
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 138
cacctcaagc tttcttagatc agctagcgac ccagccaaac tccccct 46

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized Amplification Primer Design based on EST Sequence

GenBank Accession Number AA281296

<400> 139
gcagcacaca tgcgtgaaac ctgt 24

<210> 140
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 140
gtgtcagaga tgacgcgcag gaa 23

<210> 141
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 141
accacacactt gcctgtcctg agt 23

<210> 142
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 142
actggatcct tgacaattaa tgcatacggt cgtataatgt gtggagggtt gcggagggtg 60
ggc 63

<210> 143
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 143
ctgttaatacg actcactata gggttgcgga gggtggc 38

<210> 144
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 144
cacctgcaga catgcgttcc gtcctcacgg actcatcagg ccagctggcg acgcatgtgt 60
gagccgagtc ctg 73

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 145
ggatccgccc cagagcacccg tctg 24

<210> 146
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 146
cgaagcttcc agtggccgg catctgaac 29

<210> 147
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 147
cgaagcttcc acaggcccaag cccaaactcc 29

<210> 148
<211> 26
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 148

gcggatccag agccacgtcc tacgtc

26

<210> 149

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Amplification Primer Design based on EST Sequence
GenBank Accession Number AA281296

<400> 149

gcggatccgt tcagatgccg gccccac

26

<210> 150

<211> 9

<212> PRT

<213> Homo sapiens

<400> 150

Pro Glu Met Glu Pro Pro Arg Arg Pro
1 5

<210> 151

<211> 4

<212> PRT

<213> Homo sapiens

<400> 151

Ala Ala Glu His
1

<210> 152

<211> 6

<212> PRT

<213> Homo sapiens

<400> 152

Val Gln Met Pro Ala His
1 5

<210> 153

<211> 5

<212> PRT

<213> Homo sapiens

<400> 153

Val Gly Leu Gly Leu
1 5

<210> 154

<211> 4

<212> PRT

<213> Homo sapiens

<400> 154

Arg Ala Thr Ser
1

<210> 155

<211> 622

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver.2); encoded
by SEQ ID NO:51, with Y Intron ORF3

<400> 155

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg

165	170	175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu		
180	185	190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro		
195	200	205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala		
210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser		
225	230	235
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg		
245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro		
260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly		
275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		
305	310	315
320		
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln		
325	330	335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp		
340	345	350
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser		
355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
400		
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg		

465

470

475

480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr
485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp
500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe
515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp
530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
610 615 620

CONSERV